

Genome and Metagenomics Analyses of *Clavibacter nebraskensis*, the Goss's wilt Bacterial Pathogen of Corn

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Studying High Risk Plant Pathogenic Bacteria: What We Do and How?

☐ Classical techniques ☐ MLSA ☐ Genome & ☐ Fluorescent probe-based Metagenomics high-throughput & analyses portable detection tools. Identification **Population** Systematics/ Phylogeny/ monitoring **Taxonomy Phylogenomics Detection**

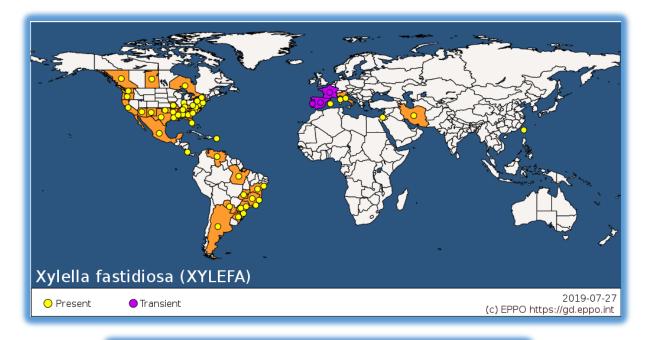
CFIA-Regulated bacteria

- ☐ One of the high-risk pathogens regulated by CFIA is *Xylella* fastidiosa.
- ☐ The bacterium Xylella fastidiosa can infect over 360 agricultural and horticultural plant species.





Pierce's disease on grapevines.



Distribution of Xylella fastidiosa in southern Ontario as determined by the polymerase chain reaction

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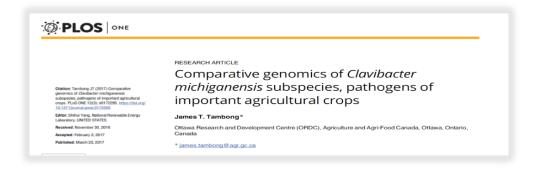
Economic Impacts of Xylella



Economic impacts

Xylella fastidiosa subsp. fastidiosa, the causal agent of Pierce's disease, has been a major constraint for grapevine production in the USA for more than 100 years, causing considerable losses. Xylella fastidiosa costs California US\$ 104 million per year in terms of losses of vines and measures for disease prevention.





Genome analysis of the Goss's bacterial wilt pathogen

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Bacteriology

Genome Analysis and Development of a Multiplex TaqMan Real-Time PCR for Specific Identification and Detection of Clavibacter michiganensis subsp. nebraskensis

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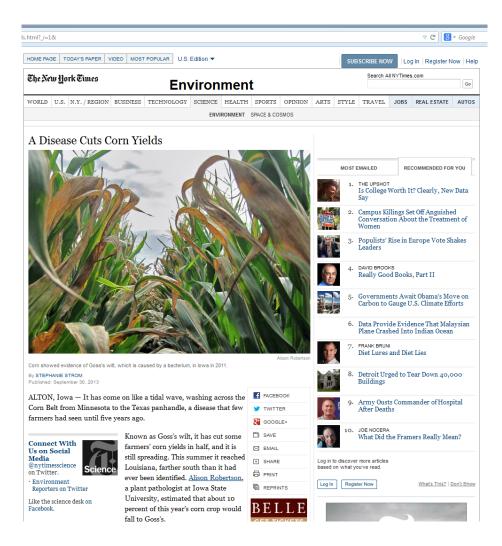
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What made the Disease "famous"?

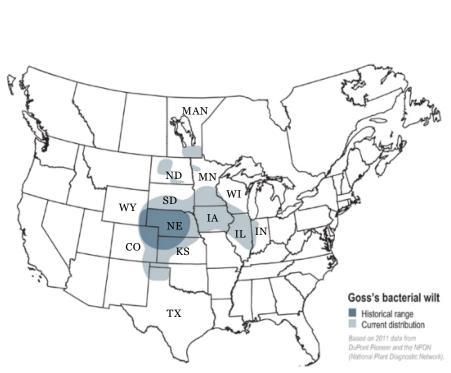
New York Times and the Goss's wilt disease of Corn?

"No one is certain why Goss's wilt has become so rampant in recent years" Stephanie Storm wrote.

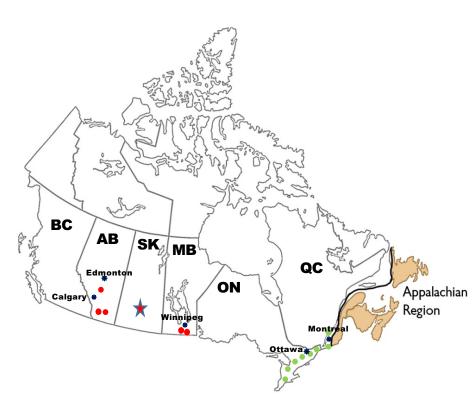


(The New York Times by Stephanie Strom, published: September 30, 2013)

Distribution of GWD: Historical and Current

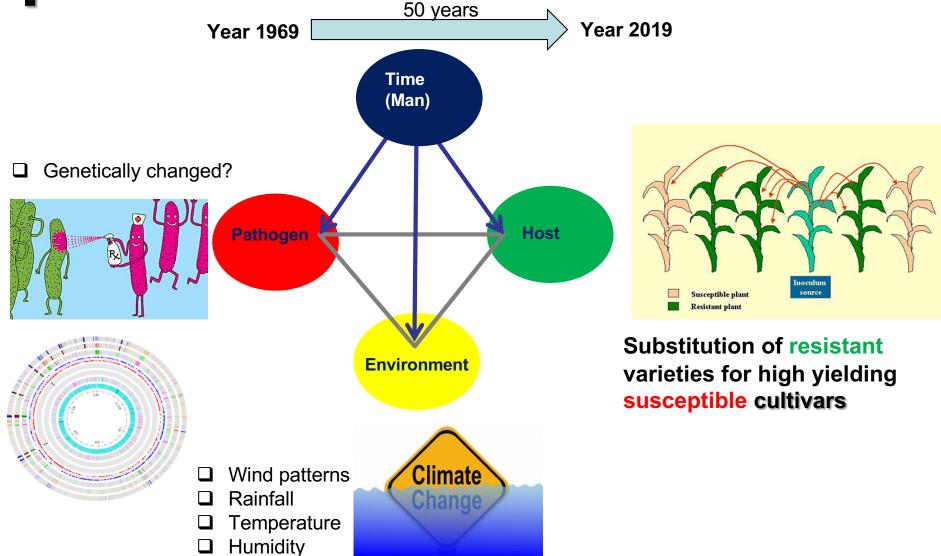


http://farmindustrynews.com/biotech-traits/growers-should-have-gosss-wilt-radar



Source: Harding et al. (2018)

Why re-emergence and rapid spread of GWD?



Basic Disease Pyramid

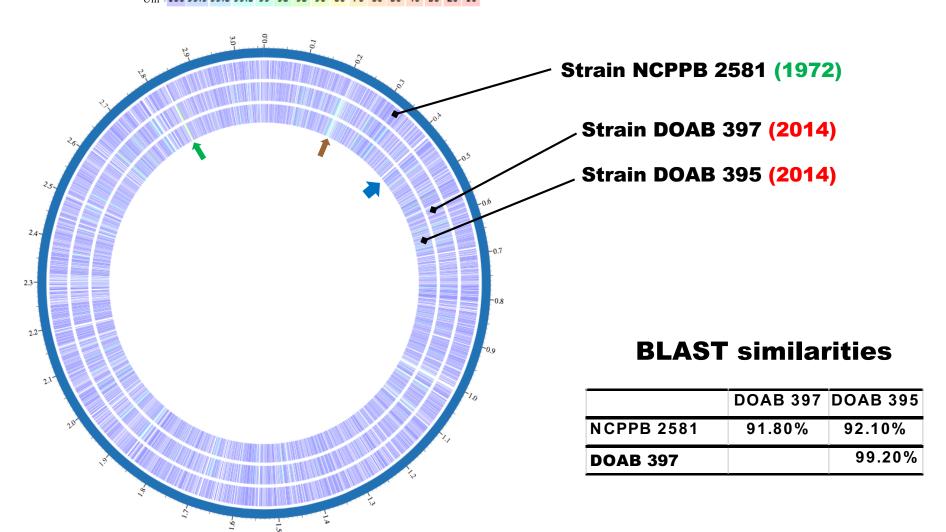
Has the GWD pathogen changed?

Proteome similarities between DOAB395 and DOAB397 to NCPPB 2581 (type

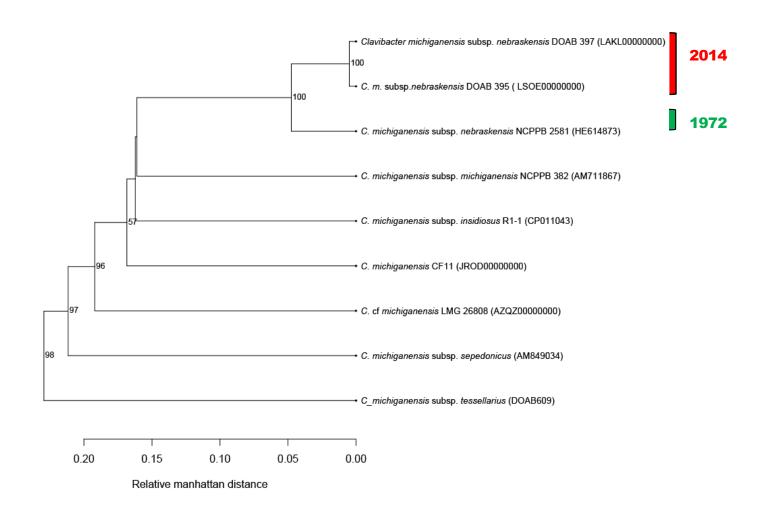
Strain)

Bi: 100 99.9 99.8 99.5 99 98 95 90 80 70 60 50 40 30 20 10

Uni: 100 99.9 99.8 99.5 99 98 95 90 80 70 60 50 40 30 20 10



Pan-genome phylogenetic tree



□ Conclusion: The 2014 Cn strains have changed genetically and should be incorporated in corn breeding programs

Nanopore-based Metagenomics analysis of Cn-infected corn leaves

Healthy

Cn-infected



Nanopore reagents



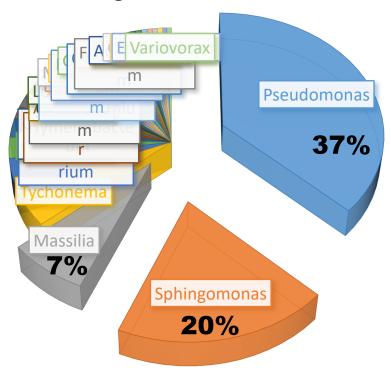
Nanopore device



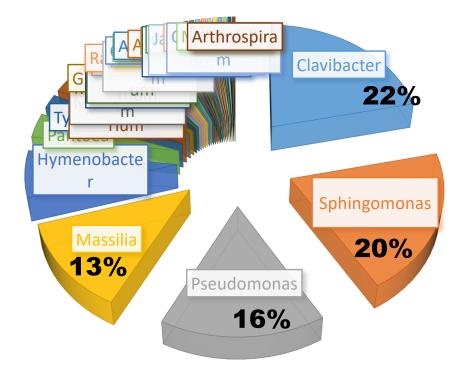
Loading sample & Sequencing

Nanopore-based metagenomics data reveal a Pseudomonas-Clavibacter population shift in Cn-infected leaves.

Healthy field corn leaves



Field infected corn leaves

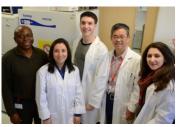


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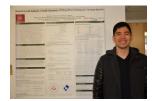
Nicole, Harini & Sean







University of Georgia, USA



Kyle

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Shima & Aissata

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Thank you / Merci!!!